

1437

atg	aca	tcg	ccc	cag	cta	gag	tgg	act	ctg	cag	acc	ctt	ctg	gag	cag	48
Met	Thr	Ser	Pro	Gln	Leu	Glu	Trp	Thr	Leu	Gln	Thr	Leu	Leu	Glu	Gln	
1				5					10					15		
ctg	aac	gag	gat	gaa	tta	aag	agt	ttc	aaa	tcc	ctt	tta	tgg	gct	ttt	96
Leu	Asn	Glu	Asp	Glu	Leu	Lys	Ser	Phe	Lys	Ser	Leu	Leu	Trp	Ala	Phe	
			20					25					30			
ccc	ctc	gaa	gac	gtg	cta	cag	aag	acc	cca	tgg	tct	gag	gtg	gaa	gag	144
Pro	Leu	Glu	Asp	Val	Leu	Gln	Lys	Thr	Pro	Trp	Ser	Glu	Val	Glu	Glu	
		35					40					45				
gct	gat	ggc	aag	aaa	ctg	gca	gaa	att	ctg	gtc	aac	acc	tcc	tca	gaa	192
Ala	Asp	Gly	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Val	Asn	Thr	Ser	Ser	Glu	
	50					55					60					
aat	tgg	ata	agg	aat	gcg	act	gtg	aac	atc	ttg	gaa	gag	atg	aat	ctc	240
Asn	Trp	Ile	Arg	Asn	Ala	Thr	Val	Asn	Ile	Leu	Glu	Glu	Met	Asn	Leu	
65					70				75					80		
acg	gaa	ttg	tgt	aag	atg	gca	aag	gct	gag	atg	atg	gag	gac	gga	cag	288
Thr	Glu	Leu	Cys	Lys	Met	Ala	Lys	Ala	Glu	Met	Met	Glu	Asp	Gly	Gln	
				85					90					95		
gtg	caa	gaa	ata	gat	aat	cct	gag	ctg	gga	gat	gca	gaa	gaa	gac	tcg	336
Val	Gln	Glu	Ile	Asp	Asn	Pro	Glu	Leu	Gly	Asp	Ala	Glu	Glu	Asp	Ser	
			100					105					110			
gag	tta	gca	aag	cca	ggc	gaa	aag	gaa	gga	tgg	aga	aat	tca	atg	gag	384
Glu	Leu	Ala	Lys	Pro	Gly	Glu	Lys	Glu	Gly	Trp	Arg	Asn	Ser	Met	Glu	
		115					120					125				
aaa	caa	tct	ttg	gtc	tgg	aag	aac	acc	ttt	tgg	caa	gga	gac	att	gac	432
Lys	Gln	Ser	Leu	Val	Trp	Lys	Asn	Thr	Phe	Trp	Gln	Gly	Asp	Ile	Asp	
	130					135					140					
aat	ttc	cat	gac	gac	gtc	act	ctg	aga	aac	caa	cgg	ttc	att	cca	ttc	480
Asn	Phe	His	Asp	Asp	Val	Thr	Leu	Arg	Asn	Gln	Arg	Phe	Ile	Pro	Phe	
145					150				155					160		
ttg	aat	ccc	aga	aca	ccc	agg	aag	cta	aca	cct	tac	acg	gtg	gtg	ctg	528
Leu	Asn	Pro	Arg	Thr	Pro	Arg	Lys	Leu	Thr	Pro	Tyr	Thr	Val	Val	Leu	
				165					170					175		
cac	ggc	ccc	gca	ggc	gtg	ggg	aaa	acc	acg	ctg	gcc	aaa	aag	tgt	atg	576
His	Gly	Pro	Ala	Gly	Val	Gly	Lys	Thr	Thr	Leu	Ala	Lys	Lys	Cys	Met	
			180					185					190			
ctg	gac	tgg	aca	gac	tgc	aac	ctc	agc	ccg	acg	ctc	aga	tac	gcg	ttc	624
Leu	Asp	Trp	Thr	Asp	Cys	Asn	Leu	Ser	Pro	Thr	Leu	Arg	Tyr	Ala	Phe	
		195					200					205				

Fig. 1A

T0E050"5E087B60

tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca	672
Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala	
210 215 220	
gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc	720
Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser	
225 230 235 240	
atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat	768
Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp	
245 250 255	
gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac	816
Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp	
260 265 270	
tgg gag aag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag	864
Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys	
275 280 285	
agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg cgg ccc agg	912
Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg	
290 295 300	
gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac ata agg	960
Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg	
305 310 315 320	
gtg gag ggc ttc ctg gag gag gac agg agg gcc tat ttc ctg aga cac	1008
Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His	
325 330 335	
ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc	1056
Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser	
340 345 350	
aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att	1104
Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile	
355 360 365	
gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccg ccg	1152
Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro	
370 375 380	
gtt ccc gca ggg cgc aca gct gcg ggg cgc gct gcg gac gct gag cct	1200
Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro	
385 390 395 400	
cct ggc cgc gca ggg ctg tgg gcg cag atg tcc gtg ttc cac cga gag	1248
Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu	
405 410 415	

Fig. 1B

gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg	1296
Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu	
420 425 430	
gac gga gac atc ctc cgc cag gag aga gtc tcc aaa ggc tgc tac tcc	1344
Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser	
435 440 445	
ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac gcc	1392
Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala	
450 455 460	
ctg gag aag gag gag gag gag gag gac agg gag ggc cac gcc tgg gac att	1440
Leu Glu Lys Glu Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile	
465 470 475 480	
ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac ccc	1488
Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro	
485 490 495	
gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag aag	1536
Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys	
500 505 510	
aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg gac	1584
Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp	
515 520 525	
atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat aag	1632
Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn Lys	
530 535 540	
ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat gag	1680
Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr Glu	
545 550 555 560	
tct cag gag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag gaa	1728
Ser Gln Glu Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys Glu	
565 570 575	
att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc ttc	1776
Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser Phe	
580 585 590	
agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta gca	1824
Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val Ala	
595 600 605	
aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att gaa	1872
Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile Glu	
610 615 620	

Fig. 1C

ttt gaa agc tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc Phe Glu Ser Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser 625 630 635 640	1920
ttc ctg agt gac tct tct gtg cgg att ctt tgt gac cac gta acc cgt Phe Leu Ser Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg 645 650 655	1968
agc acc tgt cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac Ser Thr Cys His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp 660 665 670	2016
acc gcg tac cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc Thr Ala Tyr Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu 675 680 685	2064
acg cac ctg acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met 690 695 700	2112
ctg atg ctg tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr 705 710 715 720	2160
ctg agg ttg gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe 725 730 735	2208
ttc tat gtc ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser 740 745 750	2256
gcc aat gtg ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met 755 760 765	2304
aca cgc cca aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg 770 775 780	2352
ctt aca gaa gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser 785 790 795 800	2400
aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr 805 810 815	2448
ggg gtg aag ttt ctg t Gly Val Lys Phe Leu 820	2464

Fig. 1D

09843035.050301

Qas  
Naly  
out  
TH  
ins

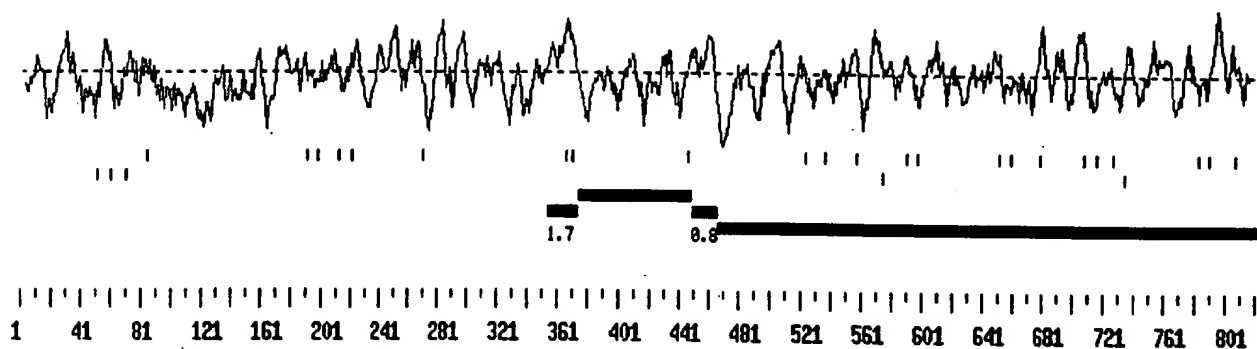


Fig. 2

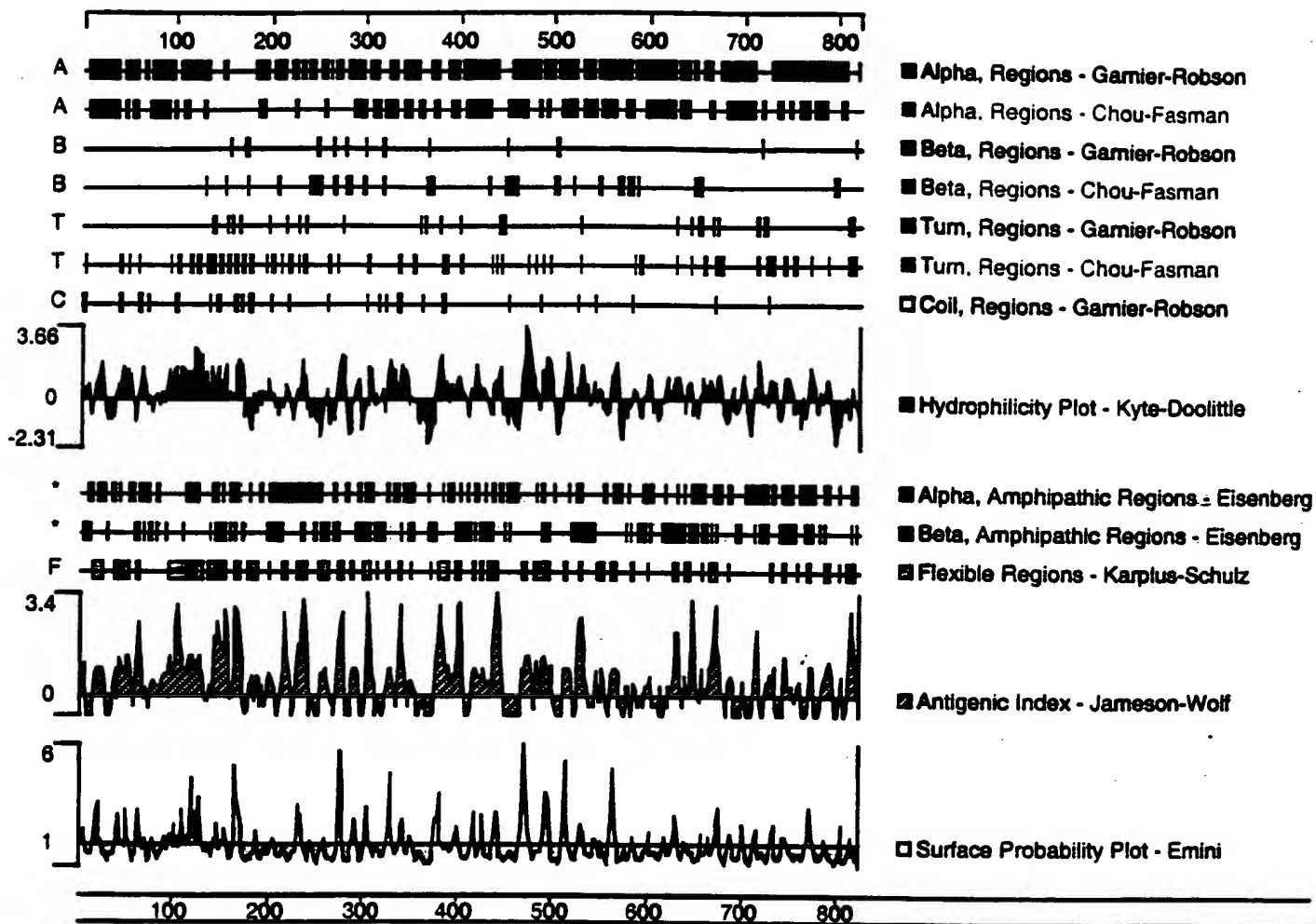


Fig. 3

NB-ARC: domain 1 of 1, from 176 to 190: score 11.4, E = 0.033

SEQID NO:9 \*->ivGMGGiGKTTLakq<-\*

++G++G+GKTTLak+

NBS-2 176 LHGPAGVGKTTLAKK 190

Fig. 4A

LRR\_RI\_2: domain 1 of 2, from 743 to 770: score 13.4, E = 0.57

SEQID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*

n+sL+ L+Ls N l deGa+ L ++ +

NBS-2 743 NQSLKHLRLSANVLLDEGAMLLYKTMTR 770

Fig. 4B

LRR\_RI\_2: domain 2 of 2, from 772 to 799: score 18.2, E = 0.12

SEQID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*

++ L+ L+L+n+ l+++ ++ La++L

NBS-2 772 KHFLQMLSLENCRLTEASCKDLAAVLVV 799

Fig. 4C

FOE050" SE084860

atg gca gaa tcg gat tct act gac ttt gac ctg ctg tgg tat cta gag	48
Met Ala Glu Ser Asp Ser Thr Asp Phe Asp Leu Leu Trp Tyr Leu Glu	
1 5 10 15	
aat ctc agt gac aag gaa ttt cag agt ttt aag aag tat ctg gca cgc	96
Asn Leu Ser Asp Lys Glu Phe Gln Ser Phe Lys Lys Tyr Leu Ala Arg	
20 25 30	
aag att ctt gat ttc aaa ctg cca cag ttt cca ctg ata cag atg aca	144
Lys Ile Leu Asp Phe Lys Leu Pro Gln Phe Pro Leu Ile Gln Met Thr	
35 40 45	
aaa gaa gaa ctg gct aac gtg ttg cca atc tct tat gag gga cag tat	192
Lys Glu Glu Leu Ala Asn Val Leu Pro Ile Ser Tyr Glu Gly Gln Tyr	
50 55 60	
ata tgg aat atg ctc ttc agc ata ttt tca atg atg cgt aag gaa gat	240
Ile Trp Asn Met Leu Phe Ser Ile Phe Ser Met Met Arg Lys Glu Asp	
65 70 75 80	
ctt tgt agg aag atc att ggc aga cga aac cat gtg ttc tac ata ctt	288
Leu Cys Arg Lys Ile Ile Gly Arg Arg Asn His Val Phe Tyr Ile Leu	
85 90 95	
caa tta gcc tat gat tct acc agc tat tat tca gca aac aat ctc aat	336
Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu Asn	
100 105 110	
gtg ttc ctg atg gga gag aga gca tct gga aaa act att gtt ata aat	384
Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile Asn	
115 120 125	
ctg gct gtg ttg agg tgg atc aag ggt gag atg tgg cag aac atg atc	432
Leu Ala Val Leu Arg Trp Ile Lys Gly Glu Met Trp Gln Asn Met Ile	
130 135 140	
tcg tac gtc gtt cac ctc act gct cac gaa ata aac cag atg acc aac	480
Ser Tyr Val Val His Leu Thr Ala His Glu Ile Asn Gln Met Thr Asn	
145 150 155 160	
agc agc ttg gct gag cta atc gcc aag gac tgg cct gac ggc cag gct	528
Ser Ser Leu Ala Glu Leu Ile Ala Lys Asp Trp Pro Asp Gly Gln Ala	
165 170 175	
ccc att gca gac atc ctg tct gat ccc aag aaa ctc ctt ttc atc ctc	576
Pro Ile Ala Asp Ile Leu Ser Asp Pro Lys Lys Leu Leu Phe Ile Leu	
180 185 190	
gag gac ttg gac aac ata aga ttc gag tta aat gtc aat gaa agt gct	624
Glu Asp Leu Asp Asn Ile Arg Phe Glu Leu Asn Val Asn Glu Ser Ala	
195 200 205	

Fig. 5A

09848035-050301



ttg tgt agt aac agc acc cag aaa gtt ccc att cca gtt ctc ctg gtc Leu Cys Ser Asn Ser Thr Gln Lys Val Pro Ile Pro Val Leu Leu Val 210 215 220	672
agt ttg ctg aag aga aaa atg gct cca ggc tgc tgg ttc ctc atc tcc Ser Leu Leu Lys Arg Lys Met Ala Pro Gly Cys Trp Phe Leu Ile Ser 225 230 235 240	720
tca agg ccc aca cgt ggg aat aat gta aaa acg ttc ttg aaa gag gta Ser Arg Pro Thr Arg Gly Asn Asn Val Lys Thr Phe Leu Lys Glu Val 245 250 255	768
gat tgc tgc acg acc ttg cag ctg tcg aat ggg aag agg gag ata tat Asp Cys Cys Thr Thr Leu Gln Leu Ser Asn Gly Lys Arg Glu Ile Tyr 260 265 270	816
ttt aac tct ttc ttt aaa gac cgc cag agg gcg tcg gca gcc ctc cag Phe Asn Ser Phe Phe Lys Asp Arg Gln Arg Ala Ser Ala Ala Leu Gln 275 280 285	864
ctt gta cat gag gat gaa ata ctc gtg ggt ctg tgc cga gtc gcc atc Leu Val His Glu Asp Glu Ile Leu Val Gly Leu Cys Arg Val Ala Ile 290 295 300	912
tta tgc tgg atc acg tgt act gtc ctg aag cgg cag atg gac aag ggg Leu Cys Trp Ile Thr Cys Thr Val Leu Lys Arg Gln Met Asp Lys Gly 305 310 315 320	960
cgt gac ttc cag ctc tgc tgc caa aca ccc act gat cta cat gcc cac Arg Asp Phe Gln Leu Cys Cys Gln Thr Pro Thr Asp Leu His Ala His 325 330 335	1008
ttt ctt gct gat gcg ttg aca tca gag gct gga ctt act gcc aat cag Phe Leu Ala Asp Ala Leu Thr Ser Glu Ala Gly Leu Thr Ala Asn Gln 340 345 350	1056
tat cac cta ggt ctc cta aaa cgt ctg tgt ttg ctg gct gca gga gga Tyr His Leu Gly Leu Leu Lys Arg Leu Cys Leu Leu Ala Ala Gly Gly 355 360 365	1104
ctg ttt ctg agc acc ctg aat ttc agt ggt gaa gac ctc aga tgt gtt Leu Phe Leu Ser Thr Leu Asn Phe Ser Gly Glu Asp Leu Arg Cys Val 370 375 380	1152
ggg ttt act gag gct gat gtc tct gtg ttg cag gcc gcg aat att ctt Gly Phe Thr Glu Ala Asp Val Ser Val Leu Gln Ala Ala Asn Ile Leu 385 390 395 400	1200
ttg ccg agc aac act cat aaa gac cgt tac aag ttc ata cac ttg aac Leu Pro Ser Asn Thr His Lys Asp Arg Tyr Lys Phe Ile His Leu Asn 405 410 415	1248

Fig. 5B

gtc cag gag ttt tgt aca gcc att gca ttt ctg atg gca gta ccc aac Val Gln Glu Phe Cys Thr Ala Ile Ala Phe Leu Met Ala Val Pro Asn 420 425 430	1296
tat ctg atc ccc tca ggc agc aga gag tat aaa gag aag aga gaa caa Tyr Leu Ile Pro Ser Gly Ser Arg Glu Tyr Lys Glu Lys Arg Glu Gln 435 440 445	1344
tac tct gac ttt aat caa gtg ttt act ttc att ttt ggt ctt cta aat Tyr Ser Asp Phe Asn Gln Val Phe Thr Phe Ile Phe Gly Leu Leu Asn 450 455 460	1392
gca aac agg aga aag att ctt gag aca tcc ttt gga tac cag cta ccg Ala Asn Arg Arg Lys Ile Leu Glu Thr Ser Phe Gly Tyr Gln Leu Pro 465 470 475 480	1440
atg gta gac agc ttc aag tgg tac tcg gtg gga tac atg aaa cat ttg Met Val Asp Ser Phe Lys Trp Tyr Ser Val Gly Tyr Met Lys His Leu 485 490 495	1488
gac cgt gac ccg gaa aag ttg acg cac cat atg cct ttg ttt tac tgt Asp Arg Asp Pro Glu Lys Leu Thr His His Met Pro Leu Phe Tyr Cys 500 505 510	1536
ctc tat gag aat cgg gaa gaa gaa ttt gtg aag acg att gtg gat gct Leu Tyr Glu Asn Arg Glu Glu Glu Phe Val Lys Thr Ile Val Asp Ala 515 520 525	1584
ctc atg gag gtt aca gtt tac ctt caa tca gac aag gat atg atg gtc Leu Met Glu Val Thr Val Tyr Leu Gln Ser Asp Lys Asp Met Met Val 530 535 540	1632
tca tta tac tgt ctg gat tac tgc tgt cac ctg agg aca ctt aag ttg Ser Leu Tyr Cys Leu Asp Tyr Cys Cys His Leu Arg Thr Leu Lys Leu 545 550 555 560	1680
agt gtt cag cgc atc ttt caa aac aaa gag cca ctt ata agg cca act Ser Val Gln Arg Ile Phe Gln Asn Lys Glu Pro Leu Ile Arg Pro Thr 565 570 575	1728
gct agt caa atg aag agc ctt gtc tac tgg aga gag atc tgc tct ctt Ala Ser Gln Met Lys Ser Leu Val Tyr Trp Arg Glu Ile Cys Ser Leu 580 585 590	1776
ttt tat aca atg gag agc ctc cgg gag ctg cat atc ttt gac aat gac Phe Tyr Thr Met Glu Ser Leu Arg Glu Leu His Ile Phe Asp Asn Asp 595 600 605	1824
ctt aat ggt att tca gaa agg att ctg tct aaa gcc ctg gag cat tct Leu Asn Gly Ile Ser Glu Arg Ile Leu Ser Lys Ala Leu Glu His Ser 610 615 620	1872

Fig. 5C

agc tgt aaa ctt cgc aca ctc aa  
Ser Cys Lys Leu Arg Thr Leu  
625 630

1895

Fig. 50

09848035-050301

0543035.05030  
2122

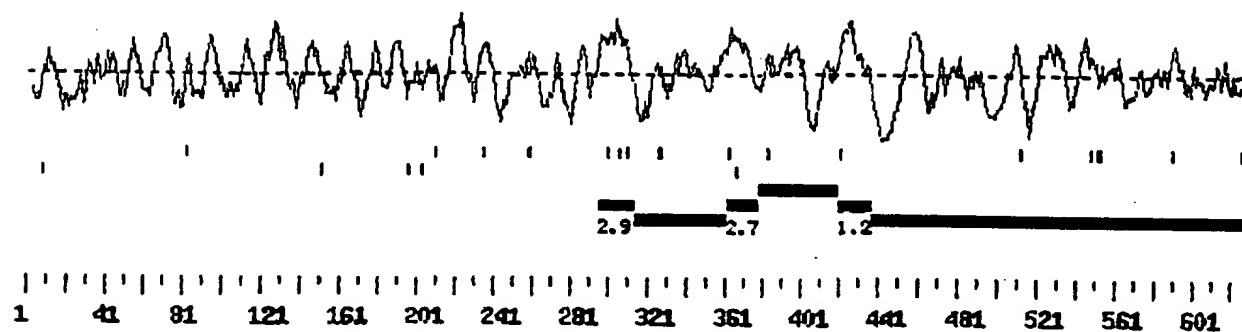


Fig. 6

09403503030

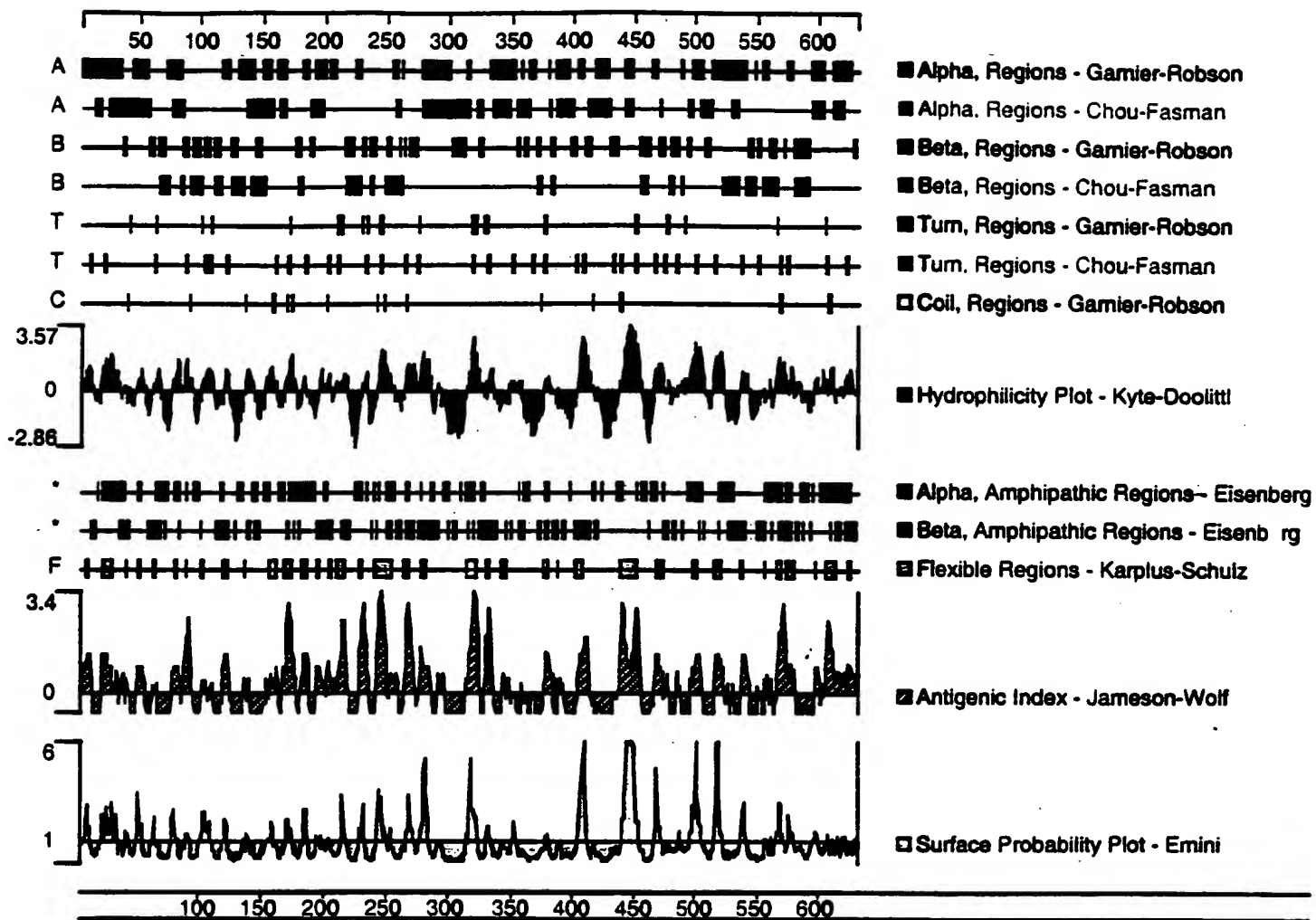


Fig. 7

09849035.050901  
TDE050"5E054B50

LRR\_R1\_2: domain 1 of 1, from 596 to 623: score 11.0, E = 1.2  
SEQ ID NO:10 \*->npsLreLdLenNklgdeGaraLaealks<-\*  
++SLreL++ +N+1 + L++aL++  
NBS-3 596 MSLRELHIFDNDLNGISERILSKALEH 623

Fig. 8

atg aag gct gaa cta ctg gag aca tgg gac aac atc agt tgg cct aaa	48
Met Lys Ala Glu Leu Leu Glu Thr Trp Asp Asn Ile Ser Trp Pro Lys	
1 5 10 15	
gac cac gta tat atc cgt aat aca tca aag gac gaa cat gag gaa ctg	96
Asp His Val Tyr Ile Arg Asn Thr Ser Lys Asp Glu His Glu Glu Leu	
20 25 30	
cag cgc cta ctg gat cct aat agg act aga gcc cag gcc cag acg ata	144
Gln Arg Leu Leu Asp Pro Asn Arg Thr Arg Ala Gln Ala Gln Thr Ile	
35 40 45	
gtc ttg gtg ggg agg gca ggg gtt ggg aag acc acc ttg gca atg cag	192
Val Leu Val Gly Arg Ala Gly Val Gly Lys Thr Thr Leu Ala Met Gln	
50 55 60	
gct atg ctg cac tgg gca aat gga gtt ctc ttt cag caa agg ttc tcc	240
Ala Met Leu His Trp Ala Asn Gly Val Leu Phe Gln Gln Arg Phe Ser	
65 70 75 80	
tat gtt ttc tat ctc agc tgc cat aaa ata agg tac atg aag gaa act	288
Tyr Val Phe Tyr Leu Ser Cys His Lys Ile Arg Tyr Met Lys Glu Thr	
85 90 95	
acc ttt gct gaa ttg att tct ttg gat tgg ccc gat ttt gat gcc ccc	336
Thr Phe Ala Glu Leu Ile Ser Leu Asp Trp Pro Asp Phe Asp Ala Pro	
100 105 110	
att gaa gag ttc atg tct caa cca gag aag ctc ctg ttt att att gat	384
Ile Glu Glu Phe Met Ser Gln Pro Glu Lys Leu Leu Phe Ile Ile Asp	
115 120 125	
ggc ttt gag gaa ata atc ata tct gag tca cgc tct gag agc ttg gat	432
Gly Phe Glu Glu Ile Ile Ile Ser Glu Ser Arg Ser Glu Ser Leu Asp	
130 135 140	
gat ggc tgc cca tgt aca gac tgg tac cag gag ctc cca gtg acc aaa	480
Asp Gly Ser Pro Cys Thr Asp Trp Tyr Gln Glu Leu Pro Val Thr Lys	
145 150 155 160	
atc cta cac agc ttg ttg aag aaa gaa ttg gtt ccc ctg gct acc tta	528
Ile Leu His Ser Leu Leu Lys Lys Glu Leu Val Pro Leu Ala Thr Leu	
165 170 175	
ctg atc acg atc aag acc tgg ttt gtg aga gat ctt aag gcc tca tta	576
Leu Ile Thr Ile Lys Thr Trp Phe Val Arg Asp Leu Lys Ala Ser Leu	
180 185 190	
gtg aat cca tgc ttt gta caa att aca ggg ttc aca ggg gac gac cta	624
Val Asn Pro Cys Phe Val Gln Ile Thr Gly Phe Thr Gly Asp Asp Leu	
195 200 205	

Fig. 9A

cgg gta tat ttc atg aga cac ttt gat gac tca agt gaa gtt gag aaa Arg Val Tyr Phe Met Arg His Phe Asp Asp Ser Ser Glu Val Glu Lys 210 215 220	672
atc ctg cag cag cta aga aaa aac gaa act ctc ttt cat tcc tgc agt Ile Leu Gln Gln Leu Arg Lys Asn Glu Thr Leu Phe His Ser Cys Ser 225 230 235 240	720
gcc ccc atg gtg tgt tgg acc gta tgt tcc tgt ctg aag cag ccg aag Ala Pro Met Val Cys Trp Thr Val Cys Ser Cys Leu Lys Gln Pro Lys 245 250 255	768
gtg agg tat tac gat ctc cag tca atc act cag act acc acc agt ctg Val Arg Tyr Tyr Asp Leu Gln Ser Ile Thr Gln Thr Thr Thr Ser Leu 260 265 270	816
tat gcc tat ttt ttc tcc aac ttg ttc tcc aca gca gag gta gat ttg Tyr Ala Tyr Phe Phe Ser Asn Leu Phe Ser Thr Ala Glu Val Asp Leu 275 280 285	864
gca gat gac agc tgg cca gga caa tgg agg gcc ctc tgc agt ctg gcc Ala Asp Asp Ser Trp Pro Gly Gln Trp Arg Ala Leu Cys Ser Leu Ala 290 295 300	912
ata gaa ggg ctg tgg tct atg aac ttc acg ttt aac aaa gaa gac act Ile Glu Gly Leu Trp Ser Met Asn Phe Thr Phe Asn Lys Glu Asp Thr 305 310 315 320	960
gag atc gag ggc ctg gaa gtg cct ttc att gat tct ctc tac gag ttc Glu Ile Glu Gly Leu Glu Val Pro Phe Ile Asp Ser Leu Tyr Glu Phe 325 330 335	1008
aat att ctt caa aag atc aat gac tgt ggg ggt tgc act act ttc acc Asn Ile Leu Gln Lys Ile Asn Asp Cys Gly Gly Cys Thr Thr Phe Thr 340 345 350	1056
cac cta agt ttc cag gag ttt ttt gca gcc atg tcc ttt gtg cta gag His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Ser Phe Val Leu Glu 355 360 365	1104
gaa cct aga gaa ttc cct ccc cat tcc aca aag cca caa gag atg aag Glu Pro Arg Glu Phe Pro Pro His Ser Thr Lys Pro Gln Glu Met Lys 370 375 380	1152
atg tta ctg caa cac gtc ttg ctt gac aaa gaa gcc tac tgg act cca Met Leu Leu Gln His Val Leu Leu Asp Lys Glu Ala Tyr Trp Thr Pro 385 390 395 400	1200
gtg gtt ctg ttc ttc ttt ggt ctt tta aat aaa aac ata gca aga gaa Val Val Leu Phe Phe Phe Gly Leu Leu Asn Lys Asn Ile Ala Arg Glu 405 410 415	1248

Fig. 9B





094300 SE034360

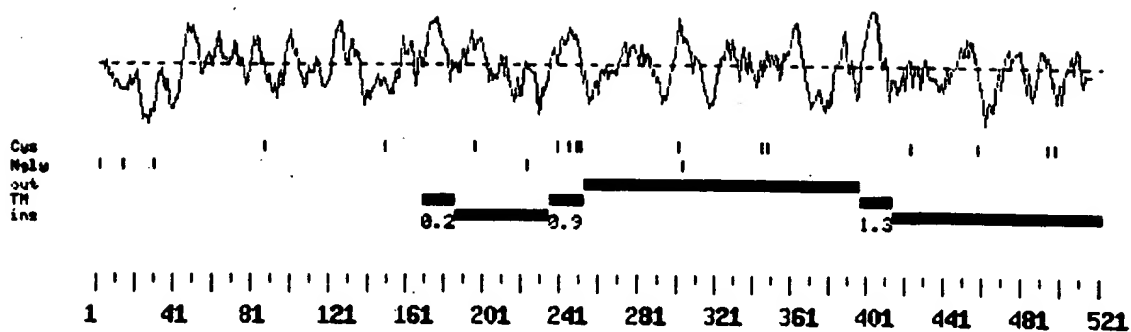


Fig. 10

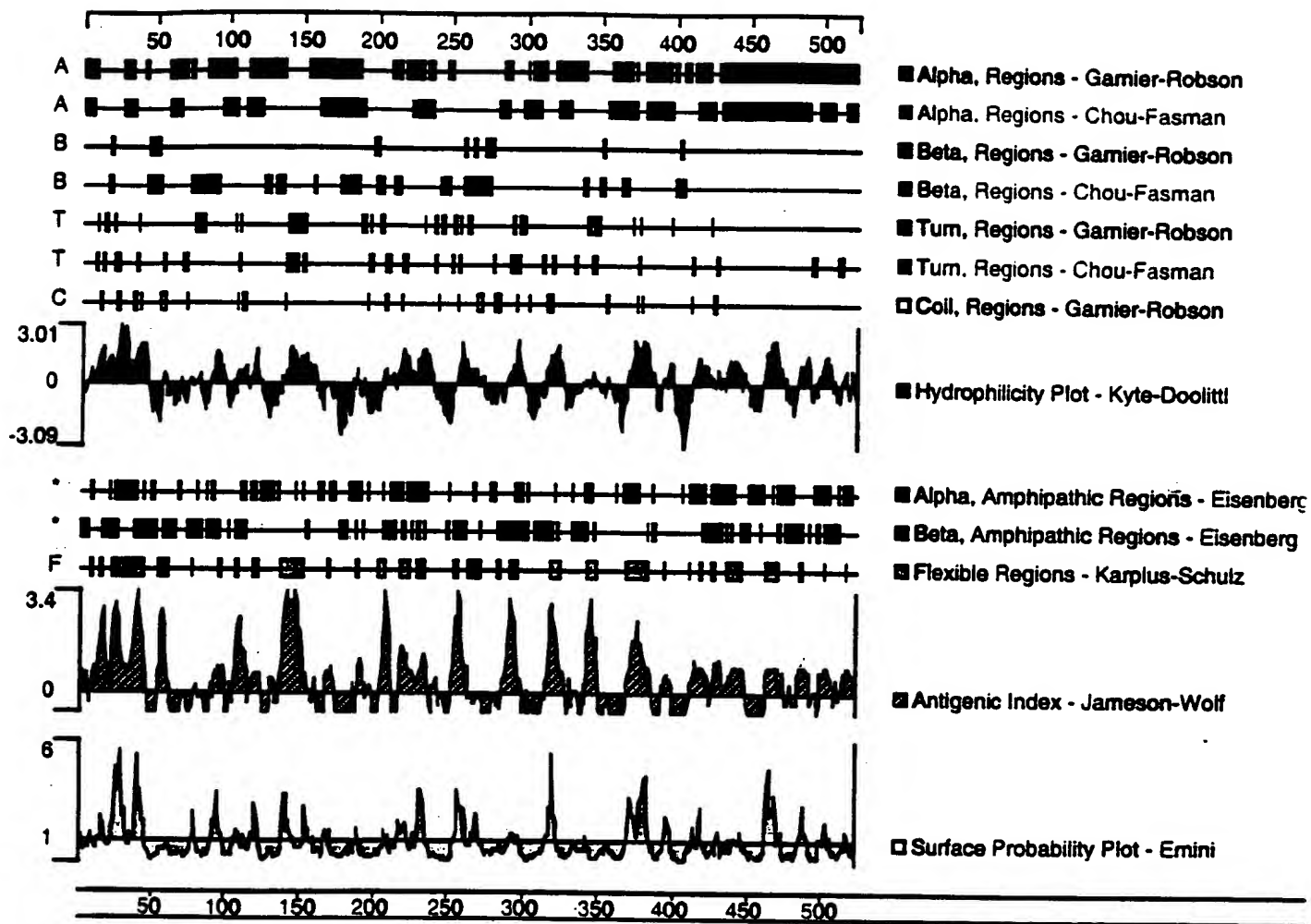


Fig. 11

09848035 050301

NB-ARC: domain 1 of 1, from 50 to 79: score 9.4, E = 0.12  
SEQIDNO: 11 \*->ivGMGGIGKTTLaqiyndes..qevqrhF<-\*  
+vG++G+GKTTLa q+ +++++ ++q +F  
NBS-4 50 LVGRAGVGKTTLAMQAMLHWangVLFOQRF 79

Fig. 1d

c agc cgc tta tgg tcc agc aag tct gtc act gag att cac cta tac ttt	49
Ser Arg Leu Trp Ser Ser Lys Ser Val Thr Glu Ile His Leu Tyr Phe	
1 5 10 15	
 gag gag gaa gtc aag caa gaa gaa tgt gac cat ttg gac cgc ctt ttt	97
Glu Glu Glu Val Lys Gln Glu Glu Cys Asp His Leu Asp Arg Leu Phe	
20 25 30	
 gct ccc aag gaa gct ggg aaa cag cca cgt aca gtg atc att caa gga	145
Ala Pro Lys Glu Ala Gly Lys Gln Pro Arg Thr Val Ile Ile Gln Gly	
35 40 45	
 cca caa gga att gga aaa acg aca ctc ctg atg aag ctg atg atg gcc	193
Pro Gln Gly Ile Gly Lys Thr Thr Leu Leu Met Lys Leu Met Met Ala	
50 55 60	
 tgg tgc gac aac aag atc ttt cgg gat agg ttc ctg tac acg ttc tat	241
Trp Ser Asp Asn Lys Ile Phe Arg Asp Arg Phe Leu Tyr Thr Phe Tyr	
65 70 75 80	
 ttc tgc tgc aga gaa ctg agg gag ttg ccg cca acg agt ttg gct gac	289
Phe Cys Cys Arg Glu Leu Arg Glu Leu Pro Pro Thr Ser Leu Ala Asp	
85 90 95	
 ttg att tcc aga gag tgg cct gac ccc gct gct cct ata aca gag atc	337
Leu Ile Ser Arg Glu Trp Pro Asp Pro Ala Ala Pro Ile Thr Glu Ile	
100 105 110	
 gtg tct caa ccg gag aga ctc ttg ttc gtc atc gac agc ttc gaa gag	385
Val Ser Gln Pro Glu Arg Leu Leu Phe Val Ile Asp Ser Phe Glu Glu	
115 120 125	
 ctg cag ggc ggc ttg aac gaa ccc gat tgc gat ctg tgt ggt gac ttg	433
Leu Gln Gly Gly Leu Asn Glu Pro Asp Ser Asp Leu Cys Gly Asp Leu	
130 135 140	
 atg gag aaa ccg ccg gtg cag gtg ctt ctg agc agt ttg ctg agg aag	481
Met Glu Lys Arg Pro Val Gln Val Leu Leu Ser Ser Leu Leu Arg Lys	
145 150 155 160	
 aag atg ctc ccg gag gcc tcc ctg ctc atc gct atc aaa ccc gtg tgc	529
Lys Met Leu Pro Glu Ala Ser Leu Leu Ile Ala Ile Lys Pro Val Cys	
165 170 175	
 ccg aag gag ctc ccg gat cag gtg acg atc tca gaa atc tac cag ccc	577
Pro Lys Glu Leu Arg Asp Gln Val Thr Ile Ser Glu Ile Tyr Gln Pro	
180 185 190	
 cgg gga ttc aac gag agt gat agg tta gtg tat ttc tgc tgt ttc ttc	625
Arg Gly Phe Asn Glu Ser Asp Arg Leu Val Tyr Phe Cys Cys Phe Phe	
195 200 205	

Fig. 13A

aaa gac ccg aaa aga gcc atg gaa gcc ttc aat ctt gta aga gaa agt Lys Asp Pro Lys Arg Ala Met Glu Ala Phe Asn Leu Val Arg Glu Ser 210 215 220	673
gaa cag ctg ttt tcc ata tgc caa atc ccg ctc ctc tgc tgg atc ctg Glu Gln Leu Phe Ser Ile Cys Gln Ile Pro Leu Leu Cys Trp Ile Leu 225 230 235 240	721
tgt acc agt ctg aag caa gag atg cag aaa gga aaa gac ctg gcc ctg Cys Thr Ser Leu Lys Gln Glu Met Gln Lys Gly Lys Asp Leu Ala Leu 245 250 255	769
acc tgc cag agc act acc tct gtg tac tcc tct ttc gtc ttt aac ctg Thr Cys Gln Ser Thr Thr Ser Val Tyr Ser Ser Phe Val Phe Asn Leu 260 265 270	817
ttc aca cct gag ggt gcc gag ggc ccg act ccg caa acc cag cac cag Phe Thr Pro Glu Gly Ala Glu Gly Pro Thr Pro Gln Thr Gln His Gln 275 280 285	865
ctg aag gcc ctg tgc tcc ctg gct gca gag ggt atg tgg aca gac aca Leu Lys Ala Leu Cys Ser Leu Ala Ala Glu Gly Met Trp Thr Asp Thr 290 295 300	913
ttt gag ttt tgt gaa gac gac ctc cgg aga aat ggg gtt gtt gac gct Phe Glu Phe Cys Glu Asp Asp Leu Arg Arg Asn Gly Val Val Asp Ala 305 310 315 320	961
gac atc cct gcg ctg ctg ggc acc aag ata ctt ctg aag tac ggg gag Asp Ile Pro Ala Leu Leu Gly Thr Lys Ile Leu Leu Lys Tyr Gly Glu 325 330 335	1009
cgt gag agc tcc tac gtg ttc ctc cac gtg tgt atc cag gag ttc tgt Arg Glu Ser Ser Tyr Val Phe Leu His Val Cys Ile Gln Glu Phe Cys 340 345 350	1057
gcc gcc ttg ttc tat ttg ctc aag agc cac ctt gat cat cct cac cca Ala Ala Leu Phe Tyr Leu Leu Lys Ser His Leu Asp His Pro His Pro 355 360 365	1105
gct gtg aga tgt gta cag gaa ttg cta gtt gcc aat ttt gaa aaa gca Ala Val Arg Cys Val Gln Glu Leu Leu Val Ala Asn Phe Glu Lys Ala 370 375 380	1153
agg aga gca cat tgg att ttt ttg ggg tgt ttt cta act ggc ctt tta Arg Arg Ala His Trp Ile Phe Leu Gly Cys Phe Leu Thr Gly Leu Leu 385 390 395 400	1201
aat aaa aag gaa caa gaa aaa ctg gat gcg ttt ttt ggc ttc caa ctg Asn Lys Lys Glu Gln Glu Lys Leu Asp Ala Phe Phe Gly Phe Gln Leu 405 410 415	1249

Fig. 13B

0904035.050301

tcc caa gag ata aag cag caa att cac cag tgc ctg aag agc tta ggg	1297
Ser Gln Glu Ile Lys Gln Gln Ile His Gln Cys Leu Lys Ser Leu Gly	
420 425 430	
gag cgt ggc aat cct cag gga cag gtg gat tcc ttg gcg ata ttt tac	1345
Glu Arg Gly Asn Pro Gln Gly Gln Val Asp Ser Leu Ala Ile Phe Tyr	
435 440 445	
tgt ctc ttt gaa atg cag gat cct gcc ttt gtg aag cag gca gtg aac	1393
Cys Leu Phe Glu Met Gln Asp Pro Ala Phe Val Lys Gln Ala Val Asn	
450 455 460	
ctc ctc caa gaa gct aac ttt cat att att gac aac gtg gac ttg gtg	1441
Leu Leu Gln Glu Ala Asn Phe His Ile Ile Asp Asn Val Asp Leu Val	
465 470 475 480	
gtt tct gcc tac tgc tta aaa tac tgc tcc agc ttg agg aaa ctc tgt	1489
Val Ser Ala Tyr Cys Leu Lys Tyr Cys Ser Ser Leu Arg Lys Leu Cys	
485 490 495	
ttt tcc gtt caa aat gtc ttt aag aaa gag gat gaa cac agc tct acg	1537
Phe Ser Val Gln Asn Val Phe Lys Lys Glu Asp Glu His Ser Ser Thr	
500 505 510	
tcg gat tac agc ctc atc tgt tgg cat cac atc tgc tct gtg ctc acc	1585
Ser Asp Tyr Ser Leu Ile Cys Trp His His Ile Cys Ser Val Leu Thr	
515 520 525	
acc agc ggg cac ctc aga gag ctc cag gtg cag gac agc acc ctc agc	1633
Thr Ser Gly His Leu Arg Glu Leu Gln Val Gln Asp Ser Thr Leu Ser	
530 535 540	
gag tcg acc ttt gtg acc tgg tgt aac cag ctg agg cat ccc agc tgt	1681
Glu Ser Thr Phe Val Thr Trp Cys Asn Gln Leu Arg His Pro Ser Cys	
545 550 555 560	
cgc ctt cag aag ctt gga ata aat aac gtt tcc ttt tct ggc cag agt	1729
Arg Leu Gln Lys Leu Gly Ile Asn Asn Val Ser Phe Ser Gly Gln Ser	
565 570 575	
gtt ctg ctc ttt gag gtg ctc ttt tat cag cca gac ttg aaa tac ctg	1777
Val Leu Leu Phe Glu Val Leu Phe Tyr Gln Pro Asp Leu Lys Tyr Leu	
580 585 590	
agc ttc acc ctc acg aaa ctc tct cgt gat gac atc agg tcc ctc tgt	1825
Ser Phe Thr Leu Thr Lys Leu Ser Arg Asp Asp Ile Arg Ser Leu Cys	
595 600 605	
gat gcc ttg aac tac cca gca ggc aac gtc aaa gag cta gcg ctg gta	1873
Asp Ala Leu Asn Tyr Pro Ala Gly Asn Val Lys Glu Leu Ala Leu Val	
610 615 620	

Fig. 13C







FOE050" SE084850

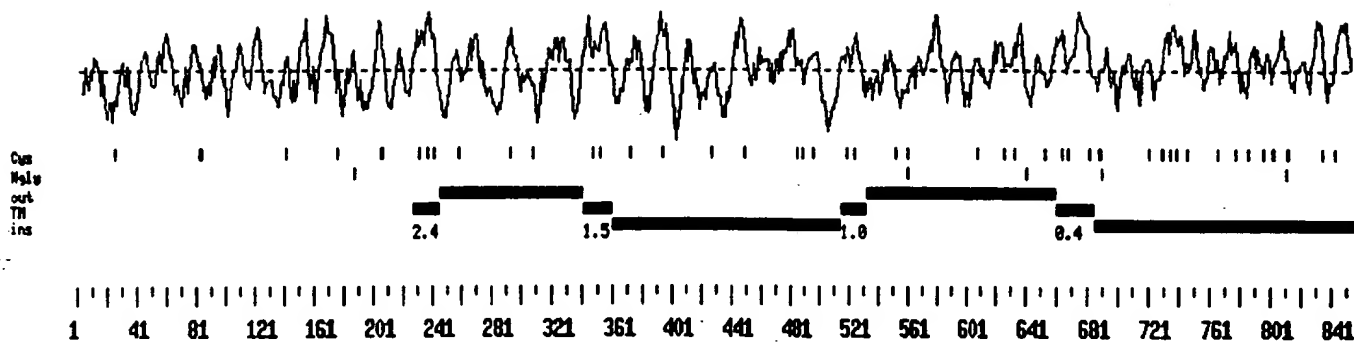


Fig. 14

004035 0530

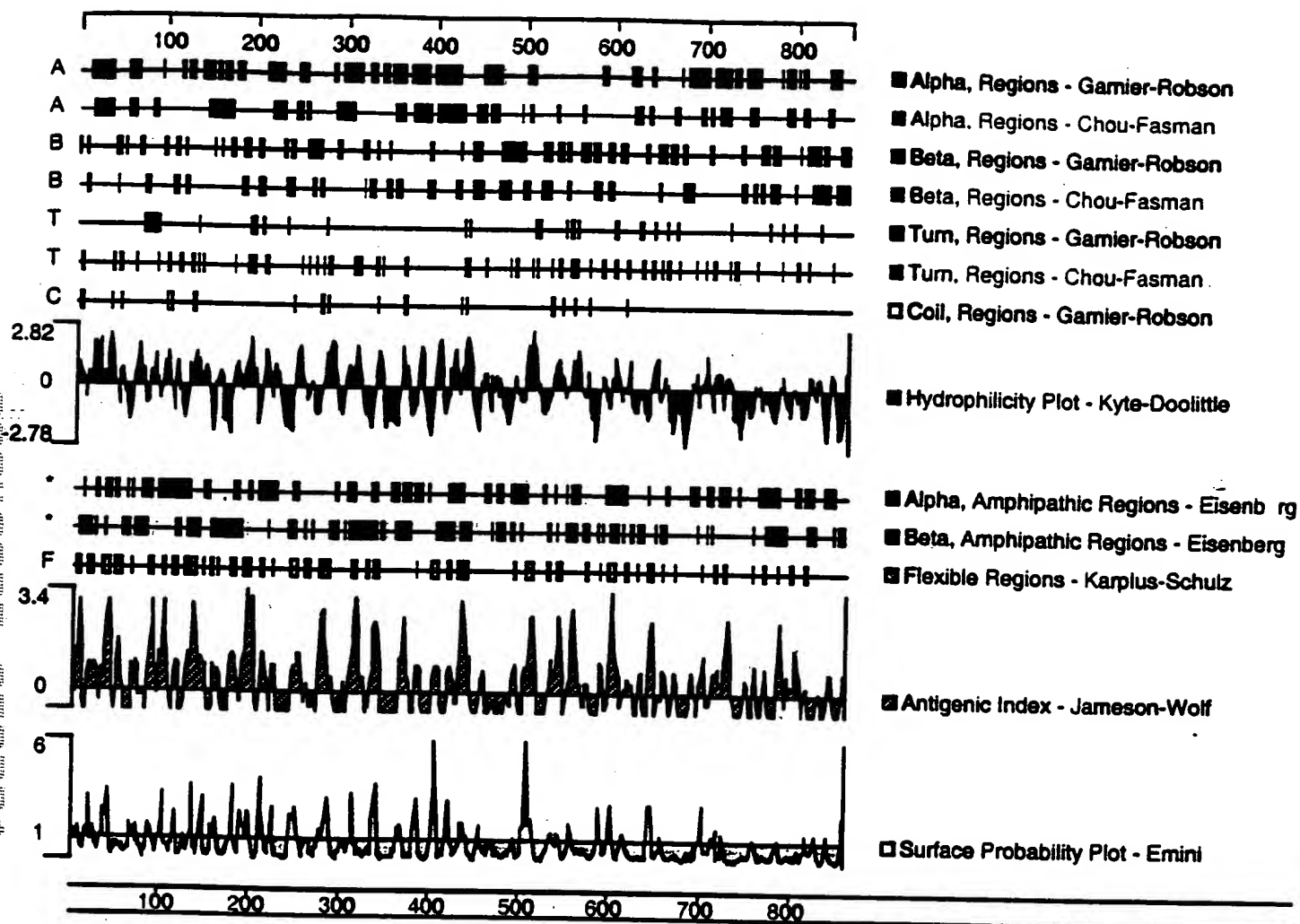


Fig. 15

LRR\_RI\_2: domain 1 of 8, from 530 to 557: score 6.4, E = 5.6  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 + +LreL++++ +l ++ ++ L++  
 NBS-5 530 SGHLRELQVQDSTLSESTFVTWCNQLRH 557

LRR\_RI\_2: domain 2 of 8, from 615 to 642: score 5.2, E = 8.4  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 + +eL L n++l + + +La +L+  
 NBS-5 615 AGNVKELALVNCHLSPIDCEVLGLLTN 642

LRR\_RI\_2: domain 3 of 8, from 643 to 669: score 9.3, E = 2.2  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 n++L L++s+N l d G+ L+eaL s  
 NBS-5 643 NKKLTYLNVSCNQL-DTGVPLLCALCS 669

LRR\_RI\_2: domain 4 of 8, from 699 to 726: score 32.8, E = 7.9e-06  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 n+s r LdLs N l deG + L+eaLk+  
 NBS-5 699 NKSVMRYLDLSANVLKDEGLKTLCEALKH 726

LRR\_RI\_2: domain 5 of 8, from 728 to 755: score 10.0, E = 1.8  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 ++L L L + +++G+ La+aL s  
 NBS-5 728 DCCLDSLCLVKCFITAAGCEDLASALIS 755

LRR\_RI\_2: domain 6 of 8, from 756 to 783: score 30.9, E = 3e-05  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 n++L+ L++++N +gd G++ L+ aL++  
 NBS-5 756 NQNLKILQIGCNEIGDVGVLCCRALTH 783

LRR\_RI\_2: domain 7 of 8, from 785 to 812: score 8.0, E = 3.3  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 ++L+ L L+ ++l+ ++ La++L+  
 NBS-5 785 DCRLEILGLEECGLTSTCKDLASVLTC 812

LRR\_RI\_2: domain 8 of 8, from 813 to 840: score 17.6, E = 0.14  
 SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
 +++L+ L+L N+l G+ +L+eaL++  
 NBS-5 813 SKFLQQLNLTLNTLDHTGVVVLCEALRH 840

Fig. 16A

Fig. 16B

Fig. 16C

Fig. 16D

Fig. 16E

Fig. 16F

Fig. 16G

Fig. 16H

gaattcgaat	tcggggaagt	tcttcagcct	taacctaaagg	tctcatactc	ggagcact	58										
atg	aca	tcg	ccc	cag	cta	gag	tgg	act	ctg	cag	acc	ctt	ctg	gag	cag	106
Met	Thr	Ser	Pro	Gln	Leu	Glu	Trp	Thr	Leu	Gln	Thr	Leu	Leu	Glu	Gln	
1				5					10					15		
ctg	aac	gag	gat	gaa	tta	aag	agt	ttc	aaa	tcc	ctt	tta	tgg	gct	ttt	154
Leu	Asn	Glu	Asp	Glu	Leu	Lys	Ser	Phe	Lys	Ser	Leu	Leu	Trp	Ala	Phe	
			20					25					30			
ccc	ctc	gaa	gac	gtg	cta	cag	aag	acc	cca	tgg	tct	gag	gtg	gaa	gag	202
Pro	Leu	Glu	Asp	Val	Leu	Gln	Lys	Thr	Pro	Trp	Ser	Glu	Val	Glu	Glu	
		35					40					45				
gct	gat	ggc	aag	aaa	ctg	gca	gaa	att	ctg	gtc	aac	acc	tcc	tca	gaa	250
Ala	Asp	Gly	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Val	Asn	Thr	Ser	Ser	Glu	
	50					55					60					
aat	tgg	ata	agg	aat	gcg	act	gtg	aac	atc	ttg	gaa	gag	atg	aat	ctc	298
Asn	Trp	Ile	Arg	Asn	Ala	Thr	Val	Asn	Ile	Leu	Glu	Glu	Met	Asn	Leu	
65					70				75						80	
acg	gaa	ttg	tgt	aag	atg	gca	aag	gct	gag	atg	atg	gag	gac	gga	cag	346
Thr	Glu	Leu	Cys	Lys	Met	Ala	Lys	Ala	Glu	Met	Met	Glu	Asp	Gly	Gln	
				85					90					95		
gtg	caa	gaa	ata	gat	aat	cct	gag	ctg	gga	gat	gca	gaa	gaa	gac	tcg	394
Val	Gln	Glu	Ile	Asp	Asn	Pro	Glu	Leu	Gly	Asp	Ala	Glu	Glu	Asp	Ser	
			100					105						110		
gag	tta	gca	aag	cca	ggt	gaa	aag	gaa	gga	tgg	aga	aat	tca	atg	gag	442
Glu	Leu	Ala	Lys	Pro	Gly	Glu	Lys	Glu	Gly	Trp	Arg	Asn	Ser	Met	Glu	
		115					120					125				
aaa	cag	tct	ttg	gtc	tgg	aag	aac	acc	ttt	tgg	caa	gga	gac	att	gac	490
Lys	Gln	Ser	Leu	Val	Trp	Lys	Asn	Thr	Phe	Trp	Gln	Gly	Asp	Ile	Asp	
	130					135					140					
aat	ttc	cat	gac	gac	gtc	act	ctg	aga	aac	caa	cgg	ttc	att	cca	ttc	538
Asn	Phe	His	Asp	Asp	Val	Thr	Leu	Arg	Asn	Gln	Arg	Phe	Ile	Pro	Phe	
145					150				155						160	
ttg	aat	ccc	aga	aca	ccc	agg	aag	cta	aca	cct	tac	acg	gtg	gtg	ctg	586
Leu	Asn	Pro	Arg	Thr	Pro	Arg	Lys	Leu	Thr	Pro	Tyr	Thr	Val	Val	Leu	
				165					170					175		
cac	ggc	ccc	gca	ggc	gtg	ggg	aaa	acc	acg	ctg	gcc	aaa	aag	tgt	atg	634
His	Gly	Pro	Ala	Gly	Val	Gly	Lys	Thr	Thr	Leu	Ala	Lys	Lys	Cys	Met	
			180					185					190			
ctg	gac	tgg	aca	gac	tgc	aac	ctc	agc	ccg	acg	ctc	aga	tac	gcg	ttc	682
Leu	Asp	Trp	Thr	Asp	Cys	Asn	Leu	Ser	Pro	Thr	Leu	Arg	Tyr	Ala	Phe	
		195					200					205				
tac	ctc	agc	tgc	aag	gag	ctc	agc	cgc	atg	ggc	ccc	tgc	agt	ttt	gca	730
Tyr	Leu	Ser	Cys	Lys	Glu	Leu	Ser	Arg	Met	Gly	Pro	Cys	Ser	Phe	Ala	
	210					215					220					

Fig. 17A



ctg gac gga gac atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac Leu Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr 450 455 460	1450
tcc ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac Ser Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr 465 470 475 480	1498
gcc ctg gag aag gag gag ggg gag gac agg gac ggc cac gcc tgg gac Ala Leu Glu Lys Glu Glu Gly Glu Asp Arg Asp Gly His Ala Trp Asp 485 490 495	1546
atc ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac Ile Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn 500 505 510	1594
ccc gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag Pro Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu 515 520 525	1642
aag aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg Lys Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro 530 535 540	1690
gac atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat Asp Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn 545 550 555 560	1738
aag ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat Lys Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr 565 570 575	1786
gag tct cag gag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag Glu Ser Gln Glu Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys 580 585 590	1834
gaa att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc Glu Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser 595 600 605	1882
ttc agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta Phe Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val 610 615 620	1930
gca aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att Ala Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile 625 630 635 640	1978
gaa ttt gaa agg tgc act tac cta acc att ccg aac tgg gct cgg cag Glu Phe Glu Arg Cys Thr Tyr Leu Thr Ile Pro Asn Trp Ala Arg Gln 645 650 655	2026
gat ctt cgc tct ctt cgc ctc tgg aca gat ttc tgc tct ctc ttc agc Asp Leu Arg Ser Leu Arg Leu Trp Thr Asp Phe Cys Ser Leu Phe Ser 660 665 670	2074

Fig. 17C

tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc ttc ctg agt	2122
Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser Phe Leu Ser	
675 680 685	
gac tct tct gtg cgg att ctt tgt gac cac gta acc cgt agc acc tgt	2170
Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg Ser Thr Cys	
690 695 700	
cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac acc gcg tac	2218
His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp Thr Ala Tyr	
705 710 715 720	
cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc acg cac ctg	2266
Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu Thr His Leu	
725 730 735	
acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg ctg atg ctg	2314
Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met Leu Met Leu	
740 745 750	
tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac ctg agg ttg	2362
Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr Leu Arg Leu	
755 760 765	
gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc ttc tat gtc	2410
Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe Phe Tyr Val	
770 775 780	
ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca gcc aat gtg	2458
Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser Ala Asn Val	
785 790 795 800	
ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg aca cgc cca	2506
Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met Thr Arg Pro	
805 810 815	
aaa cac ttc ctg cag atg ttg tgc ttg gaa aac tgt cgt ctt aca gaa	2554
Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg Leu Thr Glu	
820 825 830	
gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc aag aag ctg	2602
Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser Lys Lys Leu	
835 840 845	
aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca ggg gtg aag	2650
Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr Gly Val Lys	
850 855 860	
ttt ctg tgt gag ggc ttg agt tac cct gat tgt aaa ctg cag acc ttg	2698
Phe Leu Cys Glu Gly Leu Ser Tyr Pro Asp Cys Lys Leu Gln Thr Leu	
865 870 875 880	
gtg tta cag caa tgc agc ata acc aag ctt ggc tgt aga tat ctc tca	2746
Val Leu Gln Gln Cys Ser Ile Thr Lys Leu Gly Cys Arg Tyr Leu Ser	
885 890 895	

Fig. 17D



gag gcg ctc caa gaa gcc tgc agc ctc aca aac ctg gac ttg agt atc	2794
Glu Ala Leu Gln Glu Ala Cys Ser Leu Thr Asn Leu Asp Leu Ser Ile	
900 905 910	
aac cag ata gct cgt gga ttg tgg att ctc tgt cag gca tta gag aat	2842
Asn Gln Ile Ala Arg Gly Leu Trp Ile Leu Cys Gln Ala Leu Glu Asn	
915 920 925	
cca aac tgt aac cta aaa cac cta cgg ttg aag acc tat gaa act aat	2890
Pro Asn Cys Asn Leu Lys His Leu Arg Leu Lys Thr Tyr Glu Thr Asn	
930 935 940	
ttg gaa atc aag aag ctg ttg gag gaa gtg aaa gaa aag aat ccc aag	2938
Leu Glu Ile Lys Lys Leu Leu Glu Glu Val Lys Glu Lys Asn Pro Lys	
945 950 955 960	
ctg act att gat tgc aat gct tcc ggg gca acg gca cct ccg tgc tgt	2986
Leu Thr Ile Asp Cys Asn Ala Ser Gly Ala Thr Ala Pro Pro Cys Cys	
965 970 975	
gac ttt ttt tgc tgagcagcct gggatcgctc tacgaattac acaggaagcg	3038
Asp Phe Phe Cys	
980	
ggattcgggt ctctaagatg tcttatgaat gcaggtcaga gggtcacatg ttaacactag	3098
agtctgtcga gaggtaggat ttgacactgg ttttctcact atttttggga gattctgcac	3158
gagtcacgca ccccttcac atgacgctat gtactttctc acagggataa taaagttaga	3218
gcactctcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa	3263

Fig. 17E

atg gca gaa tcg gat tct act gac ttt gac ctg ctg tgg tat cta gag	48
Met Ala Glu Ser Asp Ser Thr Asp Phe Asp Leu Leu Trp Tyr Leu Glu	
1 5 10 15	
aat ctc agt gac aag gaa ttt cag agt ttt aag aag tat ctg gca cgc	96
Asn Leu Ser Asp Lys Glu Phe Gln Ser Phe Lys Lys Tyr Leu Ala Arg	
20 25 30	
aag att ctt gat ttc aaa ctg cca cag ttt cca ctg ata cag atg aca	144
Lys Ile Leu Asp Phe Lys Leu Pro Gln Phe Pro Leu Ile Gln Met Thr	
35 40 45	
aaa gaa gaa ctg gct aac gtg ttg cca atc tct tat gag gga cag tat	192
Lys Glu Glu Leu Ala Asn Val Leu Pro Ile Ser Tyr Glu Gly Gln Tyr	
50 55 60	
ata tgg aat atg ctc ttc agc ata ttt tca atg atg cgt aag gaa gat	240
Ile Trp Asn Met Leu Phe Ser Ile Phe Ser Met Met Arg Lys Glu Asp	
65 70 75 80	
ctt tgt agg aag atc att ggc aga cga aac cat gtg ttc tac ata ctt	288
Leu Cys Arg Lys Ile Ile Gly Arg Arg Asn His Val Phe Tyr Ile Leu	
85 90 95	
caa tta gcc tat gat tct acc agc tat tat tca gca aac aat ctc aat	336
Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu Asn	
100 105 110	
gtg ttc ctg atg gga gag aga gca tct gga aaa act att gtt ata aat	384
Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile Asn	
115 120 125	
ctg gct gtg ttg agg tgg atc aag ggt gag atg tgg cag aac atg atc	432
Leu Ala Val Leu Arg Trp Ile Lys Gly Glu Met Trp Gln Asn Met Ile	
130 135 140	
tcg tac gtc gtt cac ctc act tct cac gaa ata aac cag atg acc aac	480
Ser Tyr Val Val His Leu Thr Ser His Glu Ile Asn Gln Met Thr Asn	
145 150 155 160	
agc agc ttg gct gag cta atc gcc aag gac tgg cct gac ggc cag gct	528
Ser Ser Leu Ala Glu Leu Ile Ala Lys Asp Trp Pro Asp Gly Gln Ala	
165 170 175	
ccc att gca gac atc ctg tct gat ccc aag aaa ctc ctt ttc att ctc	576
Pro Ile Ala Asp Ile Leu Ser Asp Pro Lys Lys Leu Leu Phe Ile Leu	
180 185 190	
gag gac ttg gac aac ata aga ttc gag tta aat gtc aat gaa agt gct	624
Glu Asp Leu Asp Asn Ile Arg Phe Glu Leu Asn Val Asn Glu Ser Ala	
195 200 205	
ttg tgt agt aac agc acc cag aaa gtt ccc att cca gtt ctc ctg gtc	672
Leu Cys Ser Asn Ser Thr Gln Lys Val Pro Ile Pro Val Leu Leu Val	
210 215 220	

Fig. 18A

agt	ttg	ctg	aag	aga	aaa	atg	gct	cca	ggc	tgc	tgg	ttc	ctc	atc	tcc	720
Ser	Leu	Leu	Lys	Arg	Lys	Met	Ala	Pro	Gly	Cys	Trp	Phe	Leu	Ile	Ser	
225					230					235					240	
tca	agg	ccc	aca	cgt	ggg	aat	aat	gta	aaa	acg	ttc	ttg	aaa	gag	gta	768
Ser	Arg	Pro	Thr	Arg	Gly	Asn	Asn	Val	Lys	Thr	Phe	Leu	Lys	Glu	Val	
				245					250					255		
gat	tgc	tgc	acg	acc	ttg	cag	ctg	tgc	aat	ggg	aag	agg	gag	ata	tat	816
Asp	Cys	Cys	Thr	Thr	Leu	Gln	Leu	Ser	Asn	Gly	Lys	Arg	Glu	Ile	Tyr	
			260					265					270			
ttt	aac	tct	ttc	ttt	aaa	gac	cgc	cag	agg	gcg	tgc	gca	gcc	ctc	cag	864
Phe	Asn	Ser	Phe	Phe	Lys	Asp	Arg	Gln	Arg	Ala	Ser	Ala	Ala	Leu	Gln	
		275					280					285				
ctt	gta	cat	gag	gat	gaa	ata	ctc	gtg	ggg	ctg	tgc	cga	gtc	gcc	atc	912
Leu	Val	His	Glu	Asp	Glu	Ile	Leu	Val	Gly	Leu	Cys	Arg	Val	Ala	Ile	
	290					295					300					
tta	tgc	tgg	atc	acg	tgt	act	gtc	ctg	aag	cgg	cag	atg	gac	aag	ggg	960
Leu	Cys	Trp	Ile	Thr	Cys	Thr	Val	Leu	Lys	Arg	Gln	Met	Asp	Lys	Gly	
305					310					315					320	
cgt	gac	ttc	cag	ctc	tgc	tgc	caa	aca	ccc	act	gat	cta	cat	gcc	cac	1008
Arg	Asp	Phe	Gln	Leu	Cys	Cys	Gln	Thr	Pro	Thr	Asp	Leu	His	Ala	His	
			325						330					335		
ttt	ctt	gct	gat	gcg	ttg	aca	tca	gag	gct	gga	ctt	act	gcc	aat	cag	1056
Phe	Leu	Ala	Asp	Ala	Leu	Thr	Ser	Glu	Ala	Gly	Leu	Thr	Ala	Asn	Gln	
			340					345					350			
tat	cac	cta	ggg	ctc	cta	aaa	cgt	ctg	tgt	ttg	ctg	gct	gca	gga	gga	1104
Tyr	His	Leu	Gly	Leu	Leu	Lys	Arg	Leu	Cys	Leu	Leu	Ala	Ala	Gly	Gly	
		355					360					365				
ctg	ttt	ctg	agc	acc	ctg	aat	ttc	agt	ggg	gaa	gac	ctc	aga	tgt	gtt	1152
Leu	Phe	Leu	Ser	Thr	Leu	Asn	Phe	Ser	Gly	Glu	Asp	Leu	Arg	Cys	Val	
	370					375					380					
ggg	ttt	act	gag	gct	gat	gtc	tct	gtg	ttg	cag	gcc	gcg	aat	att	ctt	1200
Gly	Phe	Thr	Glu	Ala	Asp	Val	Ser	Val	Leu	Gln	Ala	Ala	Asn	Ile	Leu	
385					390					395					400	
ttg	ccg	agc	aac	act	cat	aaa	gac	cgt	tac	aag	ttc	ata	cac	ttg	aac	1248
Leu	Pro	Ser	Asn	Thr	His	Lys	Asp	Arg	Tyr	Lys	Phe	Ile	His	Leu	Asn	
				405					410					415		
gtc	cag	gag	ttt	tgt	aca	gcc	att	gca	ttt	ctg	atg	gca	gta	ccc	aac	1296
Val	Gln	Glu	Phe	Cys	Thr	Ala	Ile	Ala	Phe	Leu	Met	Ala	Val	Pro	Asn	
			420					425					430			
tat	ctg	atc	ccc	tca	ggc	agc	aga	gag	tat	aaa	gag	aag	aga	gaa	caa	1344
Tyr	Leu	Ile	Pro	Ser	Gly	Ser	Arg	Glu	Tyr	Lys	Glu	Lys	Arg	Glu	Gln	
		435					440					445				

tac tct gac ttt aat caa gtg ttt act ttc att ttt ggt ctt cta aat Tyr Ser Asp Phe Asn Gln Val Phe Thr Phe Ile Phe Gly Leu Leu Asn 450 455 460	1392
gca aac agg aga aag att ctt gag aca tcc ttt gga tac cag cta ccg Ala Asn Arg Arg Lys Ile Leu Glu Thr Ser Phe Gly Tyr Gln Leu Pro 465 470 475 480	1440
atg gta gac agc ttc aag tgg tac tcg gtg gga tac atg aaa cat ttg Met Val Asp Ser Phe Lys Trp Tyr Ser Val Gly Tyr Met Lys His Leu 485 490 495	1488
gac cgt gac ccg gaa aag ttg acg cac cat atg cct ttg ttt tac tgt Asp Arg Asp Pro Glu Lys Leu Thr His His Met Pro Leu Phe Tyr Cys 500 505 510	1536
ctc tat gag aat cgg gaa gaa gaa ttt gtg aag acg att gtg gat gct Leu Tyr Glu Asn Arg Glu Glu Glu Phe Val Lys Thr Ile Val Asp Ala 515 520 525	1584
ctc atg gag gtt aca gtt tac ctt caa tca gac aag gat atg atg gtc Leu Met Glu Val Thr Val Tyr Leu Gln Ser Asp Lys Asp Met Met Val 530 535 540	1632
tca tta tac tgt ctg gat tac tgc tgt cac ctg agg aca ctt aag ttg Ser Leu Tyr Cys Leu Asp Tyr Cys Cys His Leu Arg Thr Leu Lys Leu 545 550 555 560	1680
agt gtt cag cgc atc ttt caa aac aaa gag cca ctt ata agg cca act Ser Val Gln Arg Ile Phe Gln Asn Lys Glu Pro Leu Ile Arg Pro Thr 565 570 575	1728
gct agt caa atg aag agc ctt gtc tac tgg aga gag atc tgc tct ctt Ala Ser Gln Met Lys Ser Leu Val Tyr Trp Arg Glu Ile Cys Ser Leu 580 585 590	1776
ttt tat aca atg gag agc ctc cgg gag ctg cat atc ttt gac aat gac Phe Tyr Thr Met Glu Ser Leu Arg Glu Leu His Ile Phe Asp Asn Asp 595 600 605	1824
ctt aat ggt att tca gaa agg att ctg tct aaa gcc ctg gag cat tct Leu Asn Gly Ile Ser Glu Arg Ile Leu Ser Lys Ala Leu Glu His Ser 610 615 620	1872
agc tgt aaa ctt cgc aca ctc aag ttg tcc tat gtc tcg act gct tct Ser Cys Lys Leu Arg Thr Leu Lys Leu Ser Tyr Val Ser Thr Ala Ser 625 630 635 640	1920
ggg ttt gaa gac tta ctc aag gct ttg gct cgt aat cgg agc ctg aca Gly Phe Glu Asp Leu Leu Lys Ala Leu Ala Arg Asn Arg Ser Leu Thr 645 650 655	1968
tac ctg agt atc aac tgt acg tcc att tcc cta aat atg ttt tca ctt Tyr Leu Ser Ile Asn Cys Thr Ser Ile Ser Leu Asn Met Phe Ser Leu 660 665 670	2016

Fig. 18C

ctg cat gac atc ctg cac gag ccc aca tgc caa ata agt cat ctg agc Leu His Asp Ile Leu His Glu Pro Thr Cys Gln Ile Ser His Leu Ser 675 680 685	2064
ttg atg aaa tgt gat ttg cga gcc agc gaa tgc gaa gaa atc gcc tct Leu Met Lys Cys Asp Leu Arg Ala Ser Glu Cys Glu Glu Ile Ala Ser 690 695 700	2112
ctc ctc atc agt ggc ggg agt ctg aga aaa ctg acc tta tcc agc aat Leu Leu Ile Ser Gly Gly Ser Leu Arg Lys Leu Thr Leu Ser Ser Asn 705 710 715 720	2160
ccg ctg agg agc gac ggg atg aac ata ctg tgt gat gcc ttg ctt cat Pro Leu Arg Ser Asp Gly Met Asn Ile Leu Cys Asp Ala Leu Leu His 725 730 735	2208
ccc aac tgc act ctt ata tca ctg gtt ctg tct ggc tgt ttc ttt agc Pro Asn Cys Thr Leu Ile Ser Leu Val Leu Ser Gly Cys Phe Phe Ser 740 745 750	2256
agc gat atc tgt caa tat att gcc ata gtt att gct act aat gaa aaa Ser Asp Ile Cys Gln Tyr Ile Ala Ile Val Ile Ala Thr Asn Glu Lys 755 760 765	2304
ctg agg agc ctg gag att ggg agc aac aaa ata gaa gat gca gga atg Leu Arg Ser Leu Glu Ile Gly Ser Asn Lys Ile Glu Asp Ala Gly Met 770 775 780	2352
cag ctg cta tgt ggt ggt ttg aga cat ccc aac tgc atg ttg gtg aat Gln Leu Leu Cys Gly Gly Leu Arg His Pro Asn Cys Met Leu Val Asn 785 790 795 800	2400
att ggg cta gaa gag tgc atg tta acc agt gcc tgc tgt cga tct ctt Ile Gly Leu Glu Glu Cys Met Leu Thr Ser Ala Cys Cys Arg Ser Leu 805 810 815	2448
gcc tct gtt ctt acc acc aac aaa aca cta gaa aga ctc aac ttg ctt Ala Ser Val Leu Thr Thr Asn Lys Thr Leu Glu Arg Leu Asn Leu Leu 820 825 830	2496
caa aat cac ttg ggc aat gat gga gtt gca aaa ctt ctt gag agc ttg Gln Asn His Leu Gly Asn Asp Gly Val Ala Lys Leu Leu Glu Ser Leu 835 840 845	2544
atc agc cca gat tgt gta ctt aag gta gtt ggc ttg atg gct gct gag Ile Ser Pro Asp Cys Val Leu Lys Val Val Gly Leu Met Ala Ala Glu 850 855 860	2592
aac atg gag tcc ctc att ccc agg cca gca cgc tga Asn Met Glu Ser Leu Ile Pro Arg Pro Ala Arg 865 870 875	2628

Fig. 18D